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FIGURE 1A

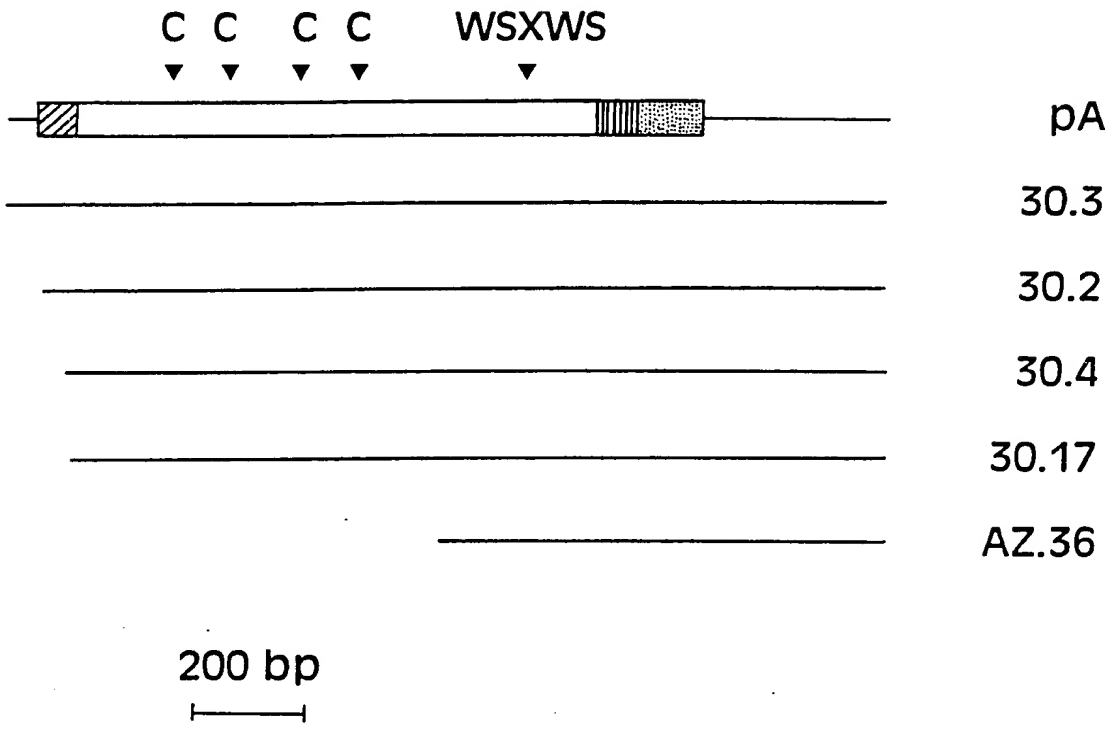

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FIGURE 2

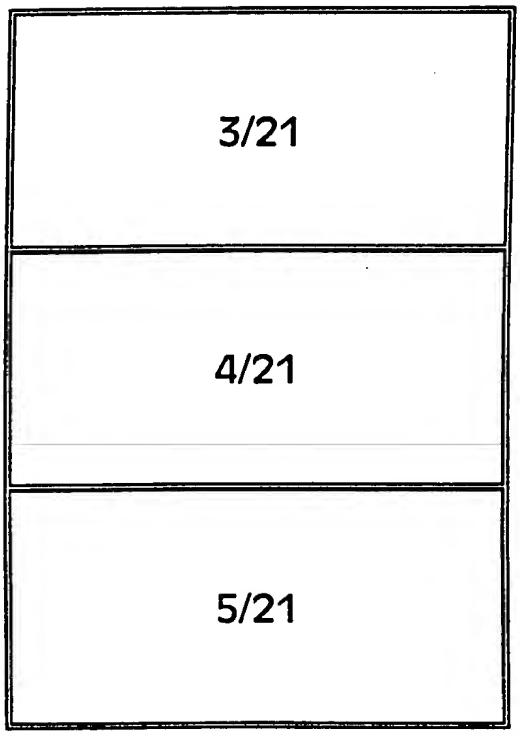

FIGURE 2

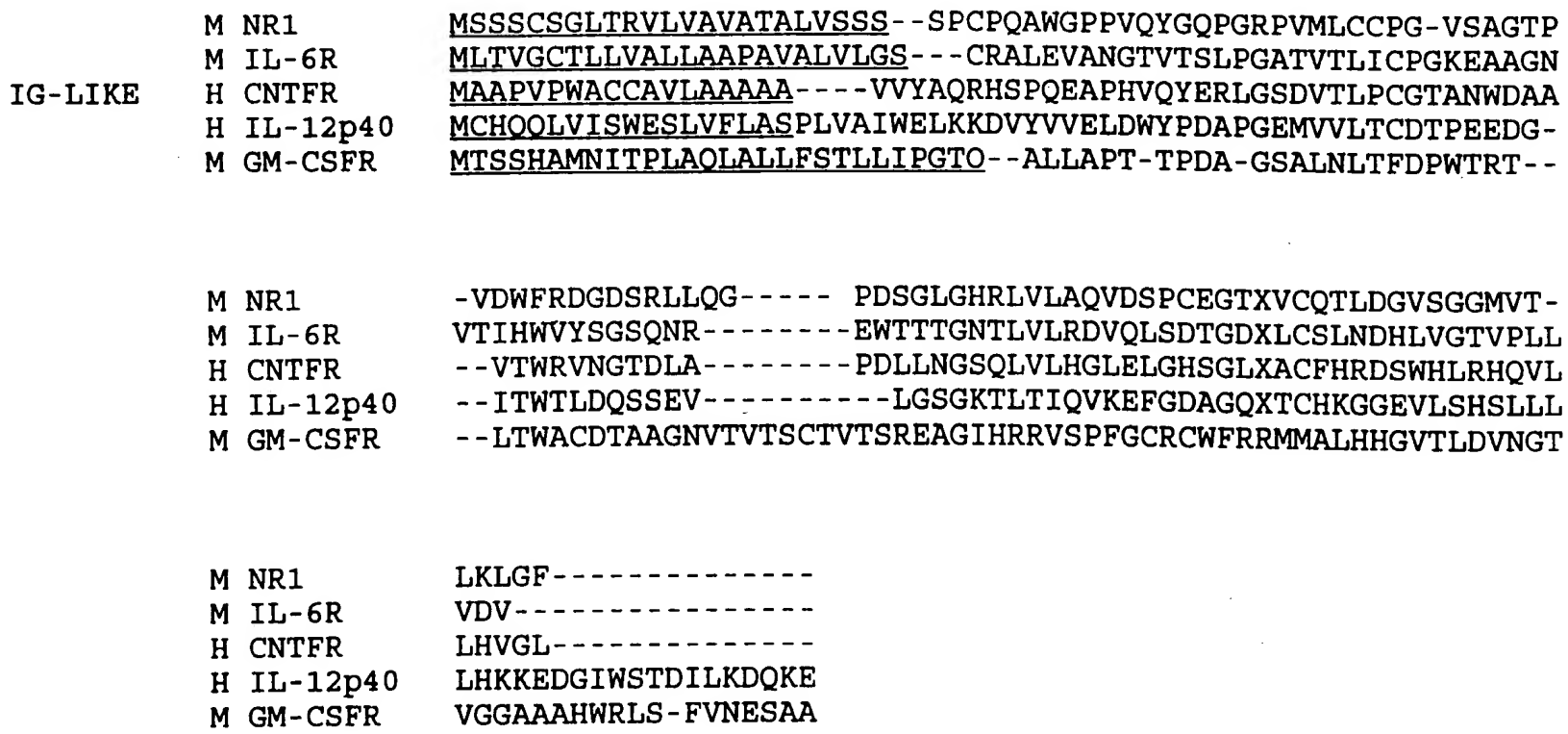

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FIGURE 2 (continued...)

	M NR1	PPARPEVSCQAVDX-EMFSCTWSPGQVSGLPTRYLTSYRKKTLPGAESQRESPSTGPWP
	M IL-6R	PPEEPKLSCFRKNPLVMAICEWRPSSTPSPTTKAVLFAKKINTTNGK------SDFQVP
SD100A	H CNTFR	PPREPVLSCRSNTXPKGFYCSWHLPTPTYIPNTFNVTVLH------------GSKIMV
	H IL-12p40	PKNKTFLRCEAKNYSGRFTCWWLTTI----STDLTFSVKSSRGSS--------DPQGVT
	M GM-CSFR	GSGAENLTCEIRAA-RFLSCAWREGPAA--PADVRYSLRVLNST---------GHDVAR

	M NR1	CPQDPLE------------ASRCVVHG----AELWSEYRTNVTEVNPL--GASTCLLD
	M IL-6R	CQYSQQLK-----------SFSCQVE-----ILEGDKVYHIVSLCVANSVGSKSSHNE
	H CNTFR	CEKDPAL------------KNRCHIRYMHLFSTIKYKVSISVSNAL----GHNATAIT
	H IL-12p40	CGAATLSAERVRGDNKEYEYSVECQEDSACPAAKESLPIEVMVDAV--HKLKYENYTSS
	M GM-CSFR	CMADPGDDV----------ITQCIA-----NDLSLLGSEAYLVVTGRSGAGPVRFLDD

	M NR1	VRLQSTLR---
	M IL-6R	AFHSLKMVQ--
	H CNTFR	FDEFTIVK---
	H IL-12p40	FFIRDIIK---
	M GM-CSFR	VVATKALERLG

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FIGURE 2 (continued...)

```
                M NR1       PDPPQGLRVESVPGYPRRLHGSWTYPASWPRQPHFL-----LKLRLQXRPAQHPAWSTV
                M IL-6R     PDPPANLVVSAIPGRPRWLKVSWQHPETWDPSY-YL-----LQFQLRXRPVWSKEFTVL
SD100B          H CNTFR     PDPPENVVARPVPSNPRRLEVTWQTPSTWPDPESFPLKFF-LRYRPLILDQWQHVELSD
                H IL-12p40  PDPPNNLQLK-PLKNSRQVEVSWEXPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTD
                M GM-CSFR   --PPRDVT---ASCNSSHCTVSWAPPSTWASLTARDFQFE-VQWQSAEPGSTPRKVLVV

                M NR1       RPIGL--EEVITDAVAGLPMAVRVSARDFLDAGTWSAWSPEAWGTPSTG-PLQDEIPD-
                M IL-6R     LLPVAQYQCVIHDALRGVKMVVQVRGKEELDLGQWSEWSPEVTGTPWIAEPRTTPAGIL
                H CNTFR     GT-----AHTITDAYAGKEYIIQVAAKDNEI-GTWSDWSVAAHATPWTEEPRHLTTEAQ
                H IL-12p40  KT--------SATVICRKNASISVRAQDRYYSSSWSEWASVPCS*
                M GM-CSFR   KETRL----AFPSPAPHGGMKVKVRAGDTRMK-HWGEWSPAHPL-EAEDTRVP------

                M NR1       WSQGHGQQLEVVVAQEDSPAPARPSLQPDPRPLDHRDPLEQ
                M IL-6R     WNPTQVSVEDSANHEDQYESSTEATSVLAPVQESSSMSLPT
                H CNTFR     AAETTTSTTSSLAPPPTTKIC--------------------
                M GM-CSF    ----------------------------------------

                M NR1       VAVLASLLGIFSCLGLAVGALALGLWLRLRRSGKDGPQKPGLLA--PMIPVEKLPGIPN
                M IL-6R     FLVAGGSLAFGLLLCVFIIL-------RLKQKWKSEAEKESKTTSPPPPPYSLGPLKPT
TM/CYT          H CNTFR     DPGELGSGGGPSAPFLVSVPITLALAAAAATASSLLI*
                M GM-CSF    ALLYAVTACAVLLCALALGVTC-----RRFEVTRR-------------LYPPIPGIRD

                M NR1       LQRTPENFS*
                M IL-6R     FLLVPLLTPHSSGSDNTVNHSCLGVRDAQSPYDNSNRDYLFPR*
                M GM-CSFR   KVSDDVRVNPETLRKDLLQP*
```

FIGURE 3

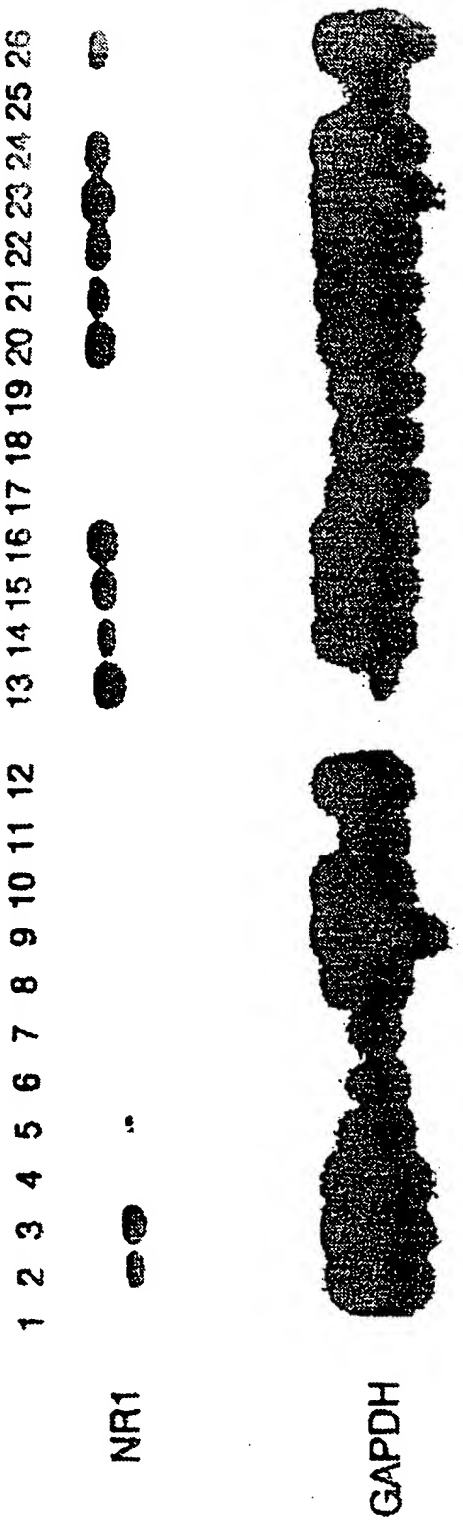
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26
NR1
GAPDH

FIGURE 4

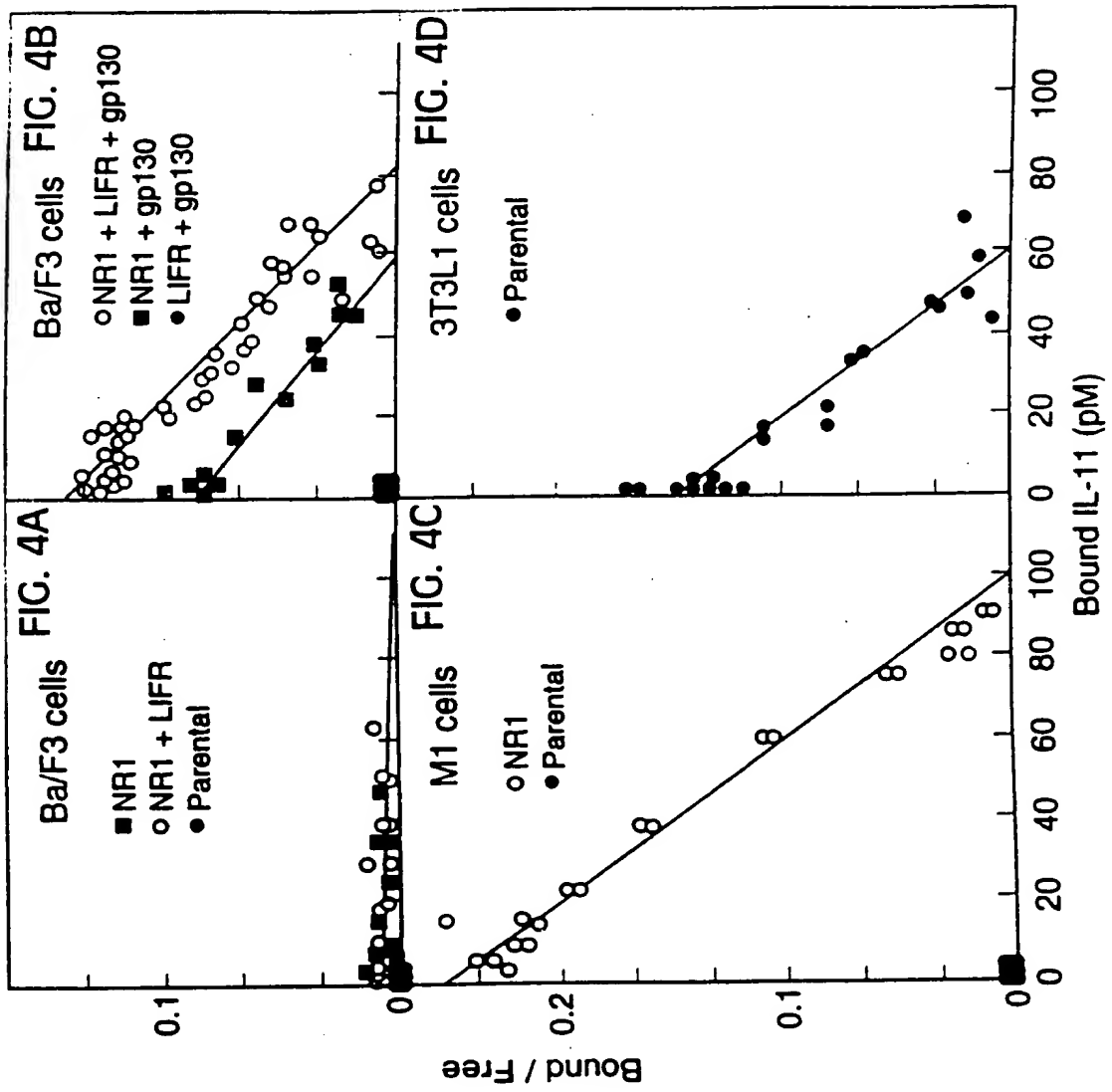
FIG. 4A
Ba/F3 cells
NR1
NR1 + LIFR
Parental
FIG. 4B
Ba/F3 cells
NR1 + LIFR + gp130
NR1 + gp130
LIFR + gp130
FIG. 4C
M1 cells
NR1
Parental
FIG. 4D
3T3L1 cells
Parental
Bound / Free
Bound IL-11 (pM)
0.1
0
0.2
0.1
0
0
20
40
60
80
100
0
20
40
60
80
100

FIGURE 5

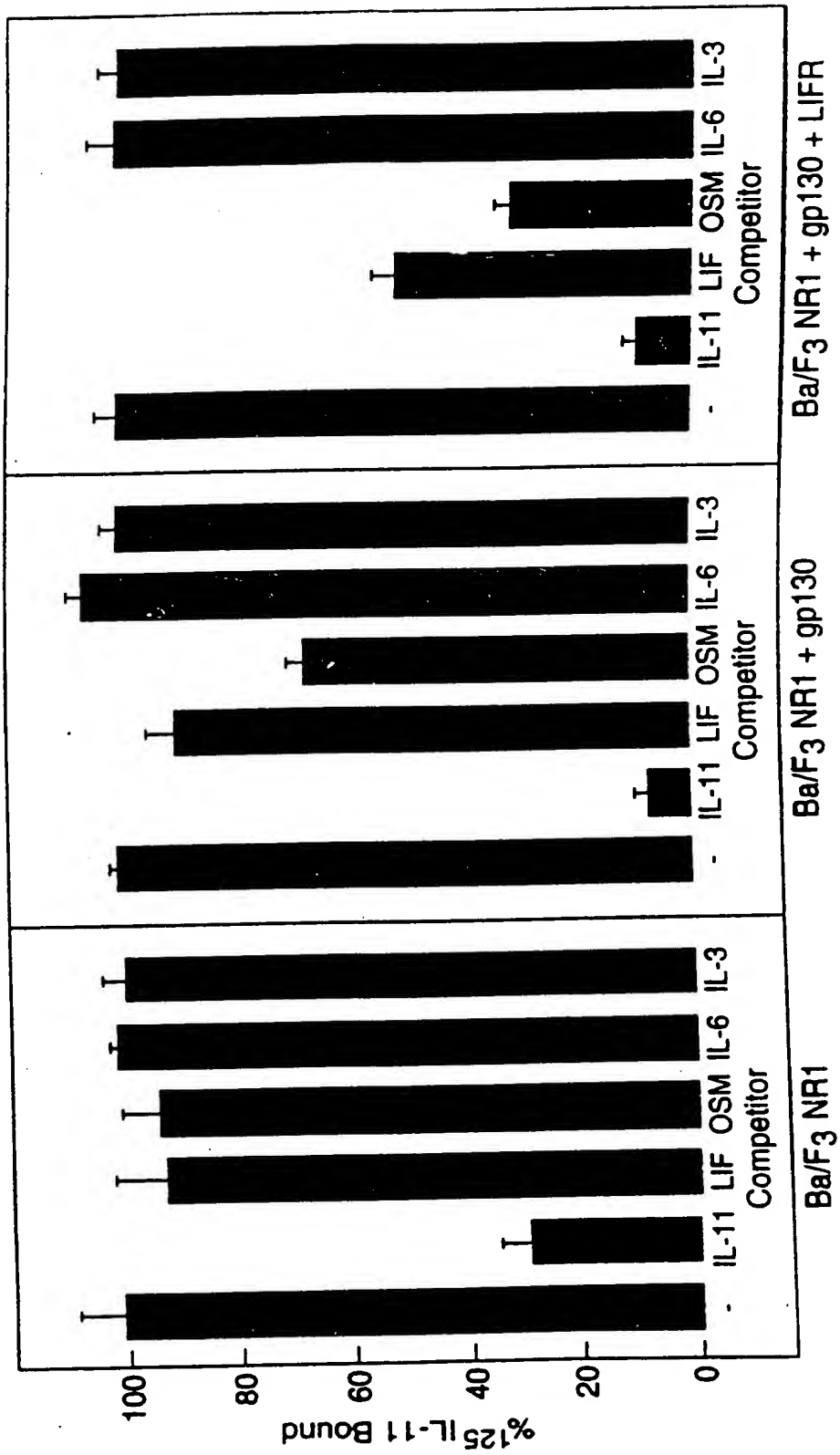
Ba/F3 NR1 + gp130 + LIFR
Ba/F3 NR1 + gp130
Ba/F3 NR1
Competitor
-
IL-11
LIF
OSM
IL-6
IL-3
% 125 IL-11 Bound
0
20
40
60
80
100

FIGURE 6

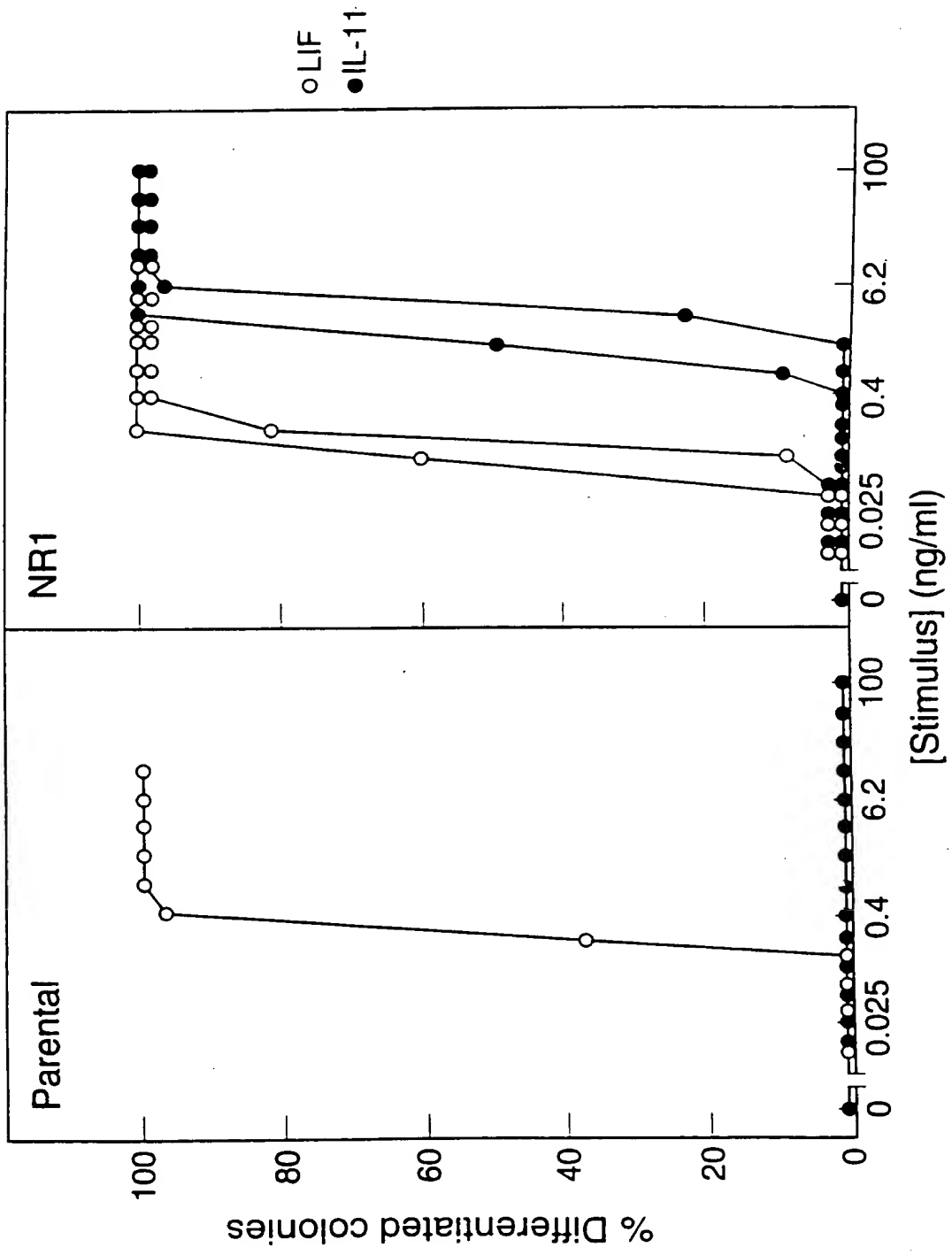
LIF
IL-11
NR1
Parental
% Differentiated colonies
100
80
60
40
20
0
0
0.025
0.4
6.2
100
[Stimulus] (ng/ml)

FIGURE 7

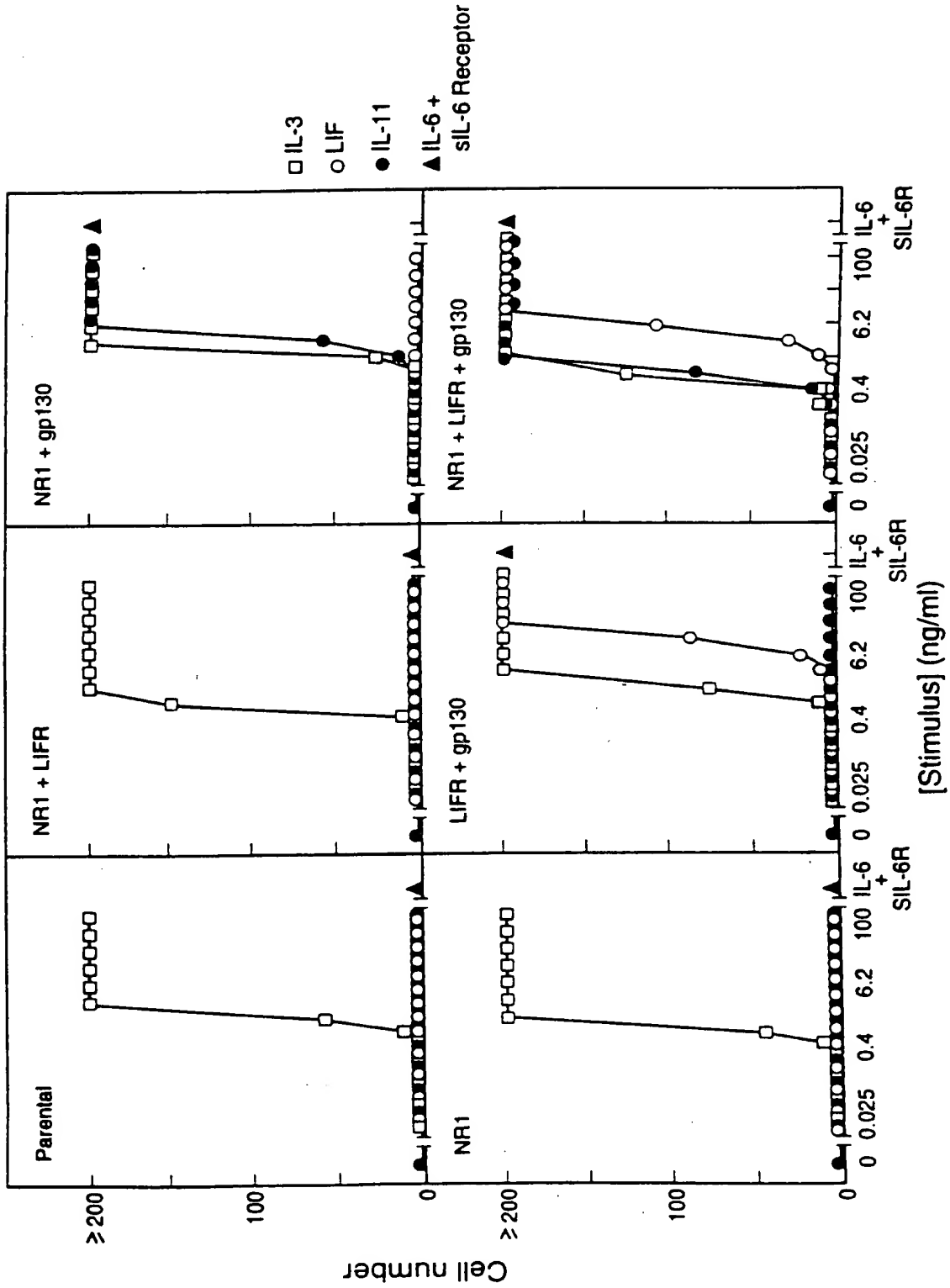
□ IL-3
○ LIF
● IL-11
▲ IL-6 + sIL-6 Receptor
Parental
NR1
NR1 + LIFR
LIFR + gp130
NR1 + gp130
NR1 + LIFR + gp130
Cell number
≥ 200
100
0
0 0.025 0.4 6.2 100 IL-6 + SIL-6R
[Stimulus] (ng/ml)

FIGURE 8

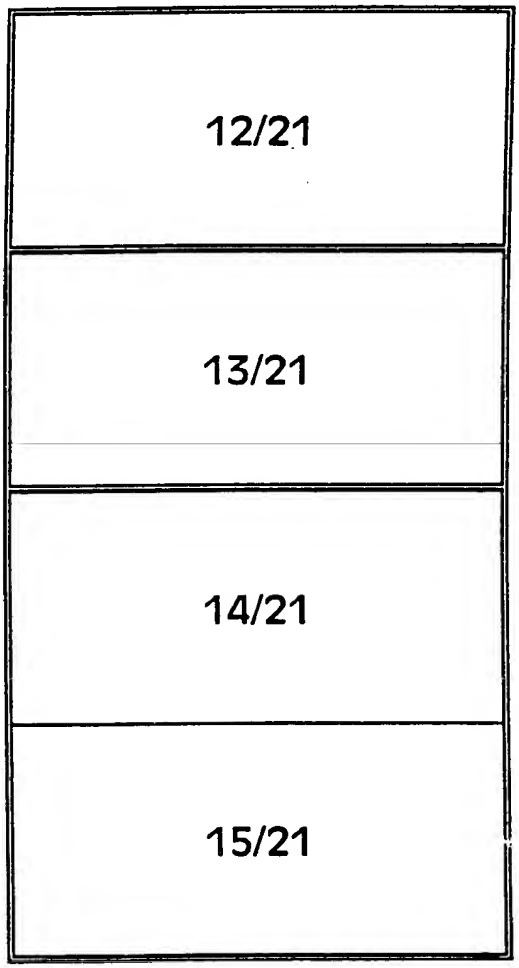

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FIGURE 8

```
TCTAACAGCC TTACCCCACT TGGTGCATCA ATTTTTCTCC TAGGAAGCCT CAGTTTTGGA      60

GAGGAAGAGC CAGGCTTTAG CTCCCATCTC AGGGGTCGGG GATTTTTGAC TCTACCTCTC     120

CCCACAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTG GTG GCC        169
        Met Ser Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala
          1               5                  10

GTG GCT ACA GCC CTG GTG TCT GCC TCC TCC CCC TGC CCC CAG GCC TGG       217
Val Ala Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala Trp
 15                  20                  25                  30

GGC CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTG AAG CTG       265
Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys Leu
                 35                  40                  45

TGT TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT CGG GAT       313
Cys Cys Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg Asp
             50                  55                  60

GGG GAG CCA AAG CTG CTC CAG GGA CCT GAC TCT GGG CTA GGG CAT GAA       361
Gly Glu Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Glu
         65                  70                  75

CTG GTC CTG GCC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC ATC TGC       409
Leu Val Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile Cys
     80                  85                  90

CAG ACC CTG GAT GGT GCA CTT GGG GGC ACA GTG ACC CTG CAG CTG GGC       457
Gln Thr Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu Gly
 95                  100                 105                 110
```

FIGURE 8

```
                                                                505
TAC CCT CCA GCC CGC CCT GTT GTC TCC TGC CAA GCA GCC GAC TAT GAG
Tyr Pro Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu
                115                 120                 125

                                                                553
AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TTA CCC ACC
Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr
            130                 135                 140

                                                                601
CGC TAC CTC ACC TCC TAC AGG AAG AAG ACA GTC CTA GGA GCT GAT AGC
Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser
        145                 150                 155

                                                                649
CAG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG GAT CCC
Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro
    160                 165                 170

                                                                697
CTA GGG GCT GCC CGC TGT GTT GTC CAC GGG GCT GAG TTC TGG AGC CAG
Leu Gly Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln
175                 180                 185                 190

                                                                745
TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTG GGT GGT GCC AGC ACA
Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Gly Gly Ala Ser Thr
                195                 200                 205

                                                                793
CGC CTG CTG GAT GTG AGC TTG CAG AGC ATC TTG CGC CCT GAC CCA CCC
Arg Leu Leu Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro
            210                 215                 220

                                                                841
CAG GGC CTG CGG GTA GAG TCA GTA CCA GGT TAC CCC CGA GGC CTG CGA
Gln Gly Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Gly Leu Arg
        225                 230                 235
```

FIGURE 8

```
GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG TGC CAG CCC CAC TTC CTG      889
Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu
  240                 245                 250

CTC AAG TTC CGT TAC CAG TTG CGT CCG GCG CAG CAT CCA GCC TGG TCC      937
Leu Lys Phe Arg Tyr Gln Leu Arg Pro Ala Gln His Pro Ala Trp Ser
255                 260                 265                 270

ACG GTG GAG CCA GCT GGA CTG GAG GAG GTG ATC ACA GAT GCT GTG GCT      985
Thr Val Glu Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala
                275                 280                 285

GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT GCT     1033
Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala
            290                 295                 300

GGC ACC TGG AGC ACC TGG AGC CCG GAG GCC TGG GGA ACT CCG AGC ACT     1081
Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr
        305                 310                 315

GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GGC CAG CTA CAC ACG CAG     1129
Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln
    320                 325                 330

CCA GAG GTG GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC TCC     1177
Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser
335                 340                 345                 350

CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG CAG     1225
Leu Gln Pro His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln
                355                 360                 365
```

FIGURE 8

```
GTA GCT GTG CTG GCG TCT TTG GGA ATC CTT TCT TTC CTG GGA CTG GTG   1273
Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val
        370                 375                 380

GCT GGG GCC CTG GCA CTG GGG CTC TGG CTG AGG CTG AGA CGG GGT GGG   1321
Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly Gly
    385                 390                 395

AAG GAT GGA TCC CCA AAG CCT GGG TTC TTG GCC TCA GTG ATT CCA GTG   1369
Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val
400                 405                 410

GAC AGG CGT CCA GGA GCT CCA AAC CTG TAGAGGACCC AGGAGGGCTT         1416
Asp Arg Arg Pro Gly Ala Pro Asn Leu
415                 420

CGGCAGATTC CACCTATAAT CCTGTCTTGC TGGTGTGGAT AGAAACCAGG CAGGACAGTA   1476

GATCCCTATG GTTGGATCTC AGCTGGAAGT TCTGTTTGGA GCCCATTTCT GTGAGACCCT   1536

GTATTTCAAA TTTGCAGCTG AAAGGTGCTT GTACCTCTGA TTTCACCCCA GAGTTGGAGT   1596

TCTGCTCAAG GAACGTGTGT AATGTGTACA TCTGTGTCCA TGTGTGACCA TGTGTCTGTG   1656

AAGCAGGGAA CATGTATTCT CTGCATGCAT GTATGTAGGT GCCTGGGGAG TGTGTGTGGG   1716

TCCTTGGCTC TTGGCCTTTC CCCTTGCAGG GGTTGTGCAG GTGTGAATAA AGAGAATAAG   1776

GAAGTTCTTG GAGATTATAC TCAG                                         1800
```

FIGURE 9

```
H1     MSSSCSGLSRVLVAVATALVSASSPCPQAWGPPGVQYGGP
M1     ********T************S*******************

H41    GRSVKLCCPGVTAGDPVSWFRDGEPKLLQGPDSGLGHELV
M41    **P*M******S**T********DSR***********R**

H81    LAQADSTDEGTYICQTLDGALGGTVTLQLGYPPARPVVSC
M81    ***V**P*****V******VS**M***K**F*****E***

H121   QAADYENFSCTWSPSQISGLPTRYLTSYRKKTVLGADSQR
M121   **V***********G*V***************LP**E***

H161   RSPSTGPWPCPQDPLGAARCVVHGAEFWSQYRINVTEVNP
M161   E**************E*S**********E**********

H201   LGGASTRLLDVSLQSILRPDPPQGLRVESVPGYPRRLRAS
M201   **#***C****R*************************H**

H241   WTYPASWPCQPHFLLKFRLQYRPAQHPAWSTVEPAGLEEV
M240   *******RR*****************************I*****

H281   ITDAVAGLPHAVRVSARDFLDAGTWSTWSPEAWGTPSTGT
M280   ***************************A***********P

H321   IPKEIPAWGQLHTQP#E#VEPQVDSPAPPRPSLQPHPRLLD
M320   LQD***D*S*G*G*QL*A*VA*E*****A******D**P**

H360   HRDSVEQVAVLASLGILSFLGLVAGALALGLWLRLRRGGK
M361   ***PL**********F*C***AV**************S**

H400   DGSPKPGFLASVIPVDRRPGAPNL
M401   **PQ***L**PM***EKL**I***QRTPENFS
```

FIGURE 10

FIG. 10A

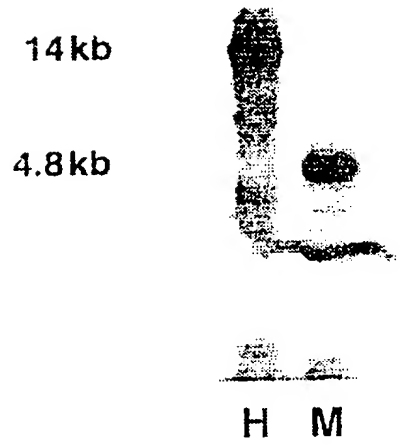

FIG. 10B

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FIGURE 11

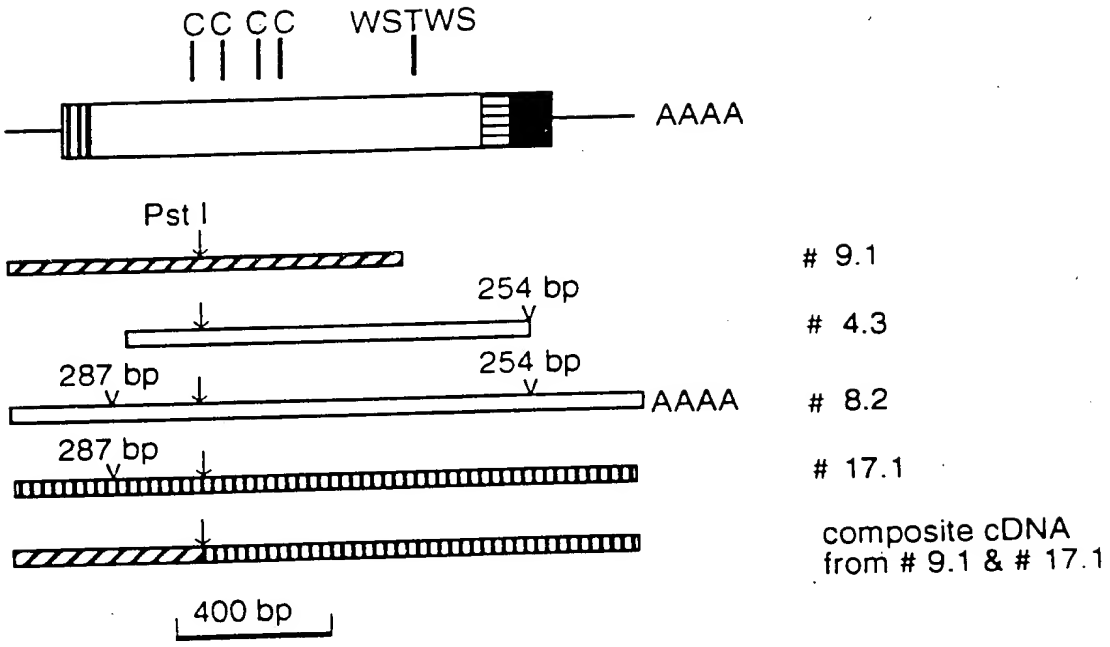
CC CC
WSTWS
AAAA
Pst I
9.1
254 bp
4.3
287 bp
254 bp
AAAA
8.2
287 bp
17.1
composite cDNA
from # 9.1 & # 17.1
400 bp

FIGURE 12

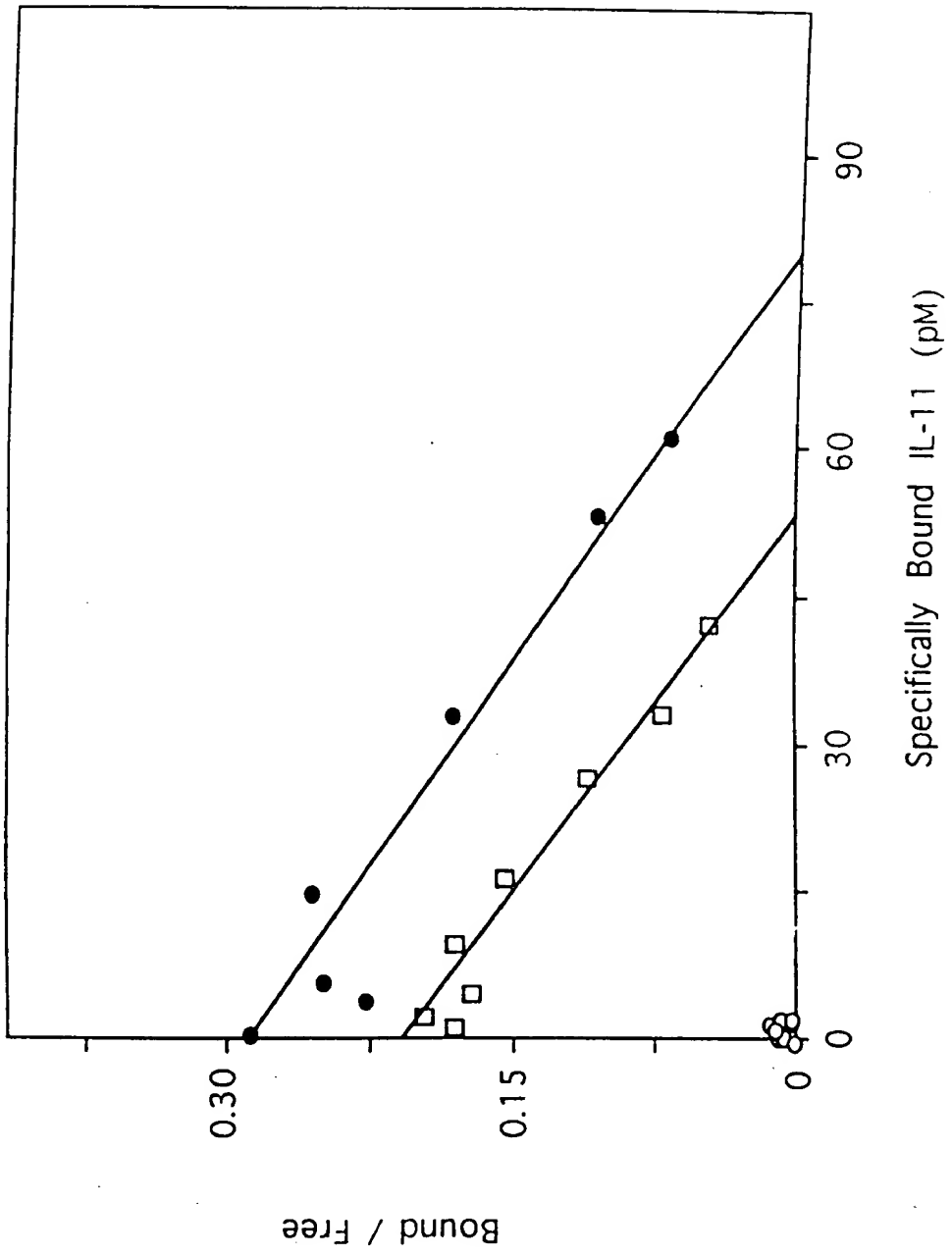

FIGURE 13

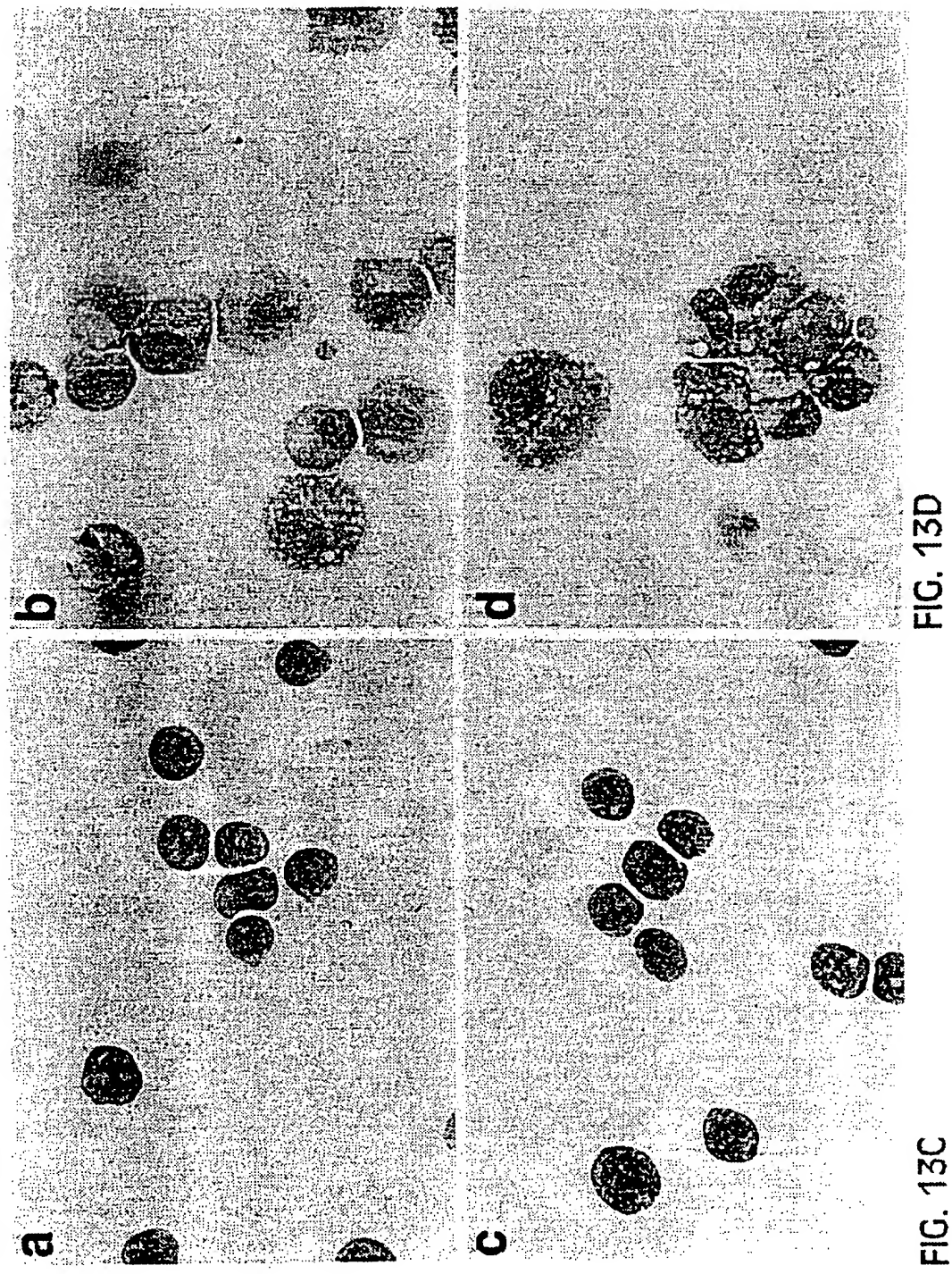

FIG. 13A FIG. 13B FIG. 13C FIG. 13D
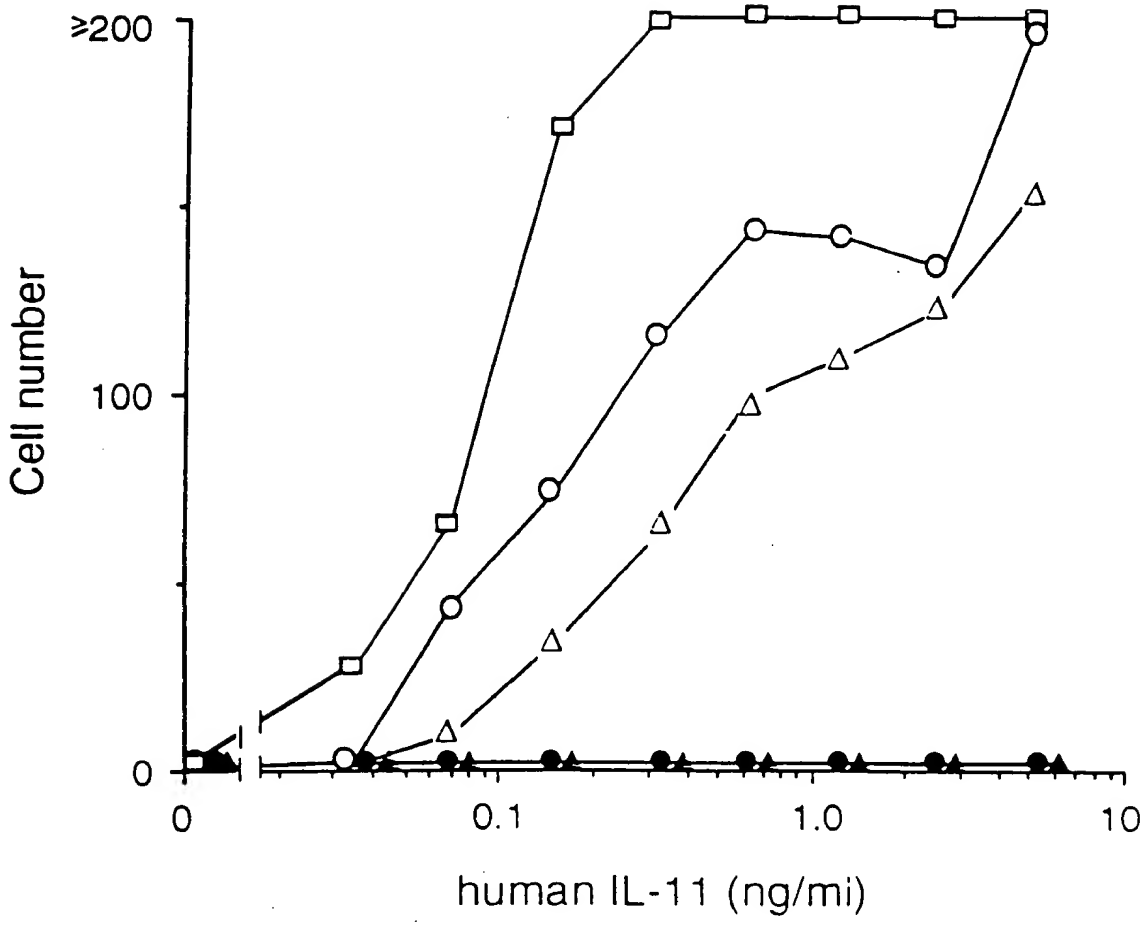
FIGURE 14